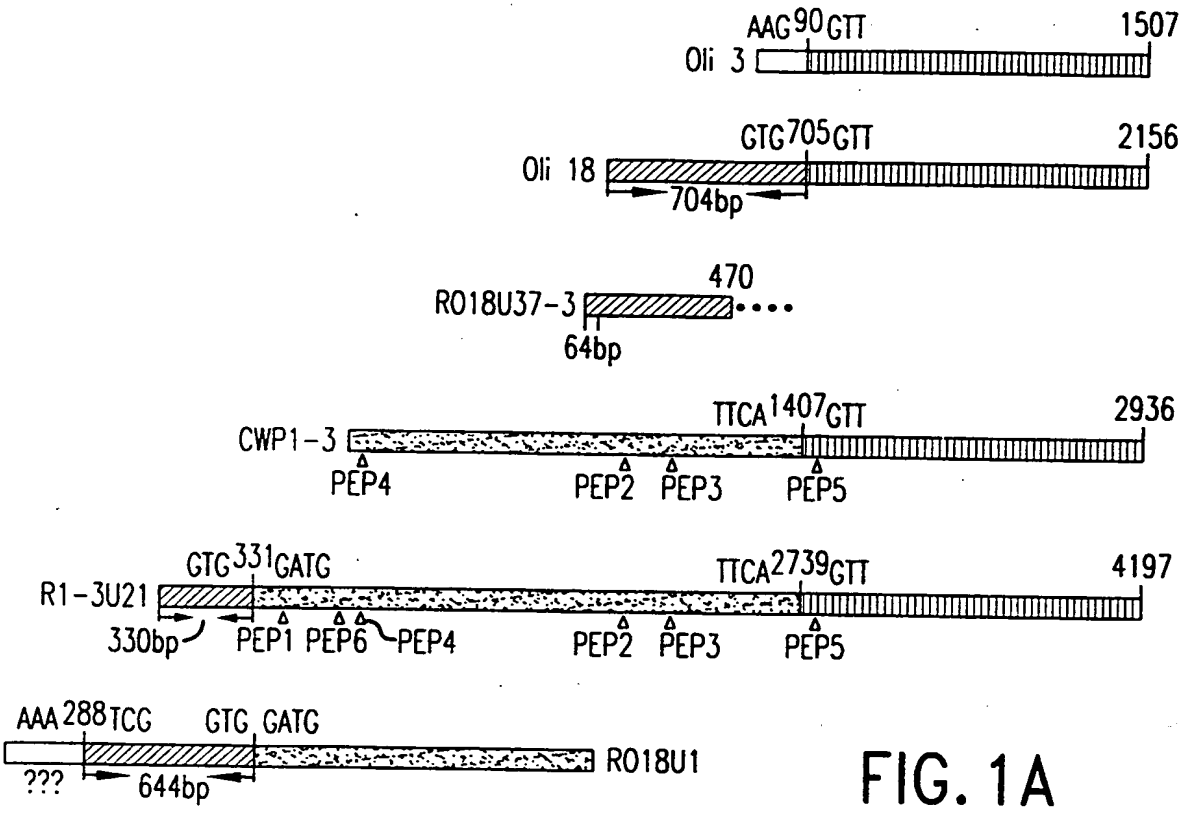

AAG 90 GTT
1507
Oli 3
GTG 705 GTT
2156
Oli 18
704bp
470
R018U37-3
64bp
TTCA 1407 GTT
2936
CWP1-3
PEP4
PEP2
PEP3
PEP5
GTG 331 GATG
TTCA 2739 GTT
4197
R1-3U21
330bp
PEP1
PEP6
PEP4
PEP2
PEP3
PEP5
AAA 288 TCG
GTG GATG
R018U1
???
644bp

FIG. 1A

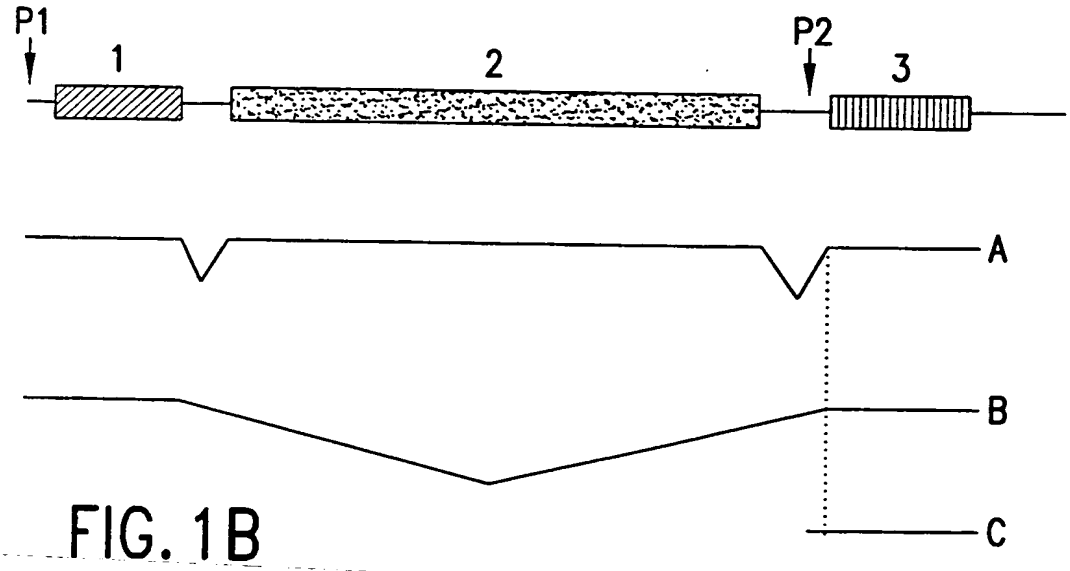

P1
1
2
P2
3
A
B
C

FIG. 1B

```
                                                ATTG CTCGTCTGGG CGGCGGCGGC GGCTGCAGCC TGGGACAGGG CGGGTGGCAC ATCTCGATCG
CGAAGGCAGG AGAAGCAGTC TCATTGTTCC GGGAGCCGTC GCCTCTGCAG GTTCTTCGGC TCGGCTCGGC ACGACTCGGC CTGCCTGGCC CCTGCCAGTC
TTGCCCAACC CCCACAACCG CCCGCGACTC TGAGGAGAAG CGGCCCTGCG GCGGCTGTAG CTGCAGCATC GTCGGCGACC CGCCAGCC(ATG)GAAGACATA
                                                                                                    M  E  D  I   4

GACCAGTCGT CGCTGGTCTC CTCGTCCACG GACAGCCCGC CCCGGCCTCC GCCCGCCTTC AAGTACCAGT TCGTGACGGA GCCCGAGGAC GAGGAGGACG
 D  Q  S  S  L  V  S  S  S  T  D  S  P  P  R  P  P  P  A  F  K  Y  Q  F  V  T  E  P  E  D  E  E  D   37
                                                                  ▲ .....

AGGAGGAGGA GGAGGACGAG GAGGAGGACG ACGAGGACCT AGAGGAACTG GAGGTGCTGG AGAGGAAGCC CGCAGCCGGG CTGTCCGCAG CTGCGGTGCC
 E  E  E  E  E  D  E  E  E  D  D  E  D  L  E  E  L  E  V  L  E  R  K  P  A  A  G  L  S  A  A  A  V   70
.....

GCCCGCCGCC GCCGCGCCGC TGCTGGACTT CAGCAGCGAC TCGGTGCCCC CCGCGCCCCG CGGGCCGCTG CCGGCCGCGC CCCCTGCCGC TCCTGAGAGG
 P  P  A  A  A  A  P  L  L  D  F  S  S  D  S  V  P  P  A  P  R  G  P  L  P  A  A  P  P  A  A  P  E  R  104

CAGCCATCCT GGGAACGCAG CCCCGCCGCG CCCGCGCCAT CCCTGCCGCC CGCTGCCGCA GTCCTGCCCT CCAAGCTCCC AGAGGACGAC GAGCCTCCGG
 Q  P  S  W  E  R  S  P  A  A  P  A  P  S  L  P  P  A  A  A  V  L  P  S  K  L  P  E  D  D  E  P  P   137

CGAGGCCCCC GCCTCCGCCG CCAGCCGCGG CGAGCCCCCT GGCGGAGCCC GCCGCGCCCC CTTCCACGCC GGCCGCGCCC AAGCGCAGGG GCTCCGGCTC
 A  R  P  P  P  P  P  P  A  G  A  S  P  L  A  E  P  A  A  P  P  S  T  P  A  A  P  K  R  R  G  S  G   170

AGTGGATGAG ACCCTTTTTG CTCTTCCTGC TGCATCTGAG CCTGTGATAC CCTCCTCTGC AGAAAAAATT ATGGATTTGA TGGAGCAGCC AGGTAACACT
 S  V  D  E  T  L  F  A  L  P  A  A  S  E  P  V  I  P  S  S  A  E  K  I  M  D  L  M  E  Q  P  G  N  T   204

GTTTCGTCTG GTCAAGAGGA TTTCCCATCT GTCCTGCTTG AAACTGCTGC CTCTCTTCCT TCTCTATCTC CTCTCTCAAC TGTTTCTTTT AAAGAACATG
 V  S  S  G  Q  E  D  F  P  S  V  L  L  E  T  A  A  S  L  P  S  L  S  P  L  S  T  V [S] F  K  E  H   237

GATACCTTGG TAACTTATCA GCAGTGTCAT CCTCAGAAGG AACAATTGAA GAAACTTTAA ATGAAGCTTC TAAAGAGTTG CCAGAGAGGG CAACAAATCC
 G  Y  L  G  N  L  S  A  V  S  S  S  E  G  T  I  E  E  T  L  N  E  A  S  K  E  L  P  E  R  A  T  N   270
```

FIG.2A1

```
ATTTGTAAAT AGAGATTTAG CAGAATTTTC AGAATTAGAA TATTCAGAAA TGGGATCATC TTTTAAAGGC TCCCCAAAAG GAGAGTCAGC CATATTAGTA
P  F  V  N  R  D  L  A  E  F  S  E  L  E  Y  S  E  M  G  S  S  F  K  G  S  P  K  G  E  S  A  I  L  V  304

GAAAACACTA AGGAAGAAGT AATTGTGAGG AGTAAAGACA AAGAGGATTT AGTTTGTAGT GCAGCCCTTC ACAGTCCACA AGAATCACCT GTGGGTAAAG
   E  N  T  K  E  E  V  I  V  R  S  K  D  K  E  D  L  V  C  S  A  A  L  H  S  P  Q  E  S  P  V  G  K  337

AAGACAGAGT TGTGTCTCCA GAAAAGACAA TGGACATTTT TAATGAAATG CAGATGTCAG TAGTAGCACC TGTGAGGGAA GAGTATGCAG ACTTTAAGCC
   E  D  R  V  V  S  P  E  K  T  M  D  I  F  N  E  M  Q  M  S  V  V  A  P  V  R  E  E  Y  A  D  F  K  370

ATTTGAACAA GCATGGGAAG TGAAAGATAC TTATGAGGGA AGTAGGGATG TGCTGGCTGC TAGAGCTAAT GTGGAAAGTA AAGTGGACAG AAAATGCTTG
P  F  E  Q  A  W  E  V  K  D  T  Y  E  G  S  R  D  V  L  A  A  R  A  N  V  E  S  K  V  D  R  K  C  I  404

GAAGATAGCC TGGAGCAAAA AAGTCTTGGG AAGGATAGTG AAGGCAGAAA TGAGGATGCT TCTTTCCCCA GTACCCCAGA ACCTGTGAAG GACAGCTCCA
   E  D  S  L  E  Q  K  S  L  G  K  D  S  E  G  R  N  E  D  A  S  F  P  S  T  P  E  P  V  K  D  S  S  437

GAGCATATAT TACCTGTGCT TCCTTTACCT CAGCAACCGA AAGCACCACA GCAAACACTT TCCCTTTGTT AGAAGATCAT ACTTCAGAAA ATAAAACAGA
   R  A  Y  I  T  C  A  S  F  T  S  A  T  E  S  T  T  A  N  T  F  P  L  L  E  D  H  T  S  E  N  K  T  470

TGAAAAAAAA ATAGAAGAAA GGAAGGCCCA AATTATAACA GAGAAGACTA GCCCCAAAAC GTCAAATCCT TTCCTTGTAG CAGTACAGGA TTCTGAGGCA
D  E  K  K  I  E  E  R  K  A  Q  I  I  T  E  K  T  S  P  K  T  S  N  P  F  L  V  A  V  Q  D  S  E  A  504

GATTATGTTA CAACAGATAC CTTATCAAAG GTGACTGAGG CAGCAGTGTC AAACATGCCT GAAGGTCTGA CGCCAGATTT AGTTCAGGAA GCATGTGAAA
   D  Y  V  T  T  D  T  L  S  K  V  T  E  A  A  V  S  N  M  P  E  G  L  T  P  D  L  V  Q  E  A  C  E  537

GTGAACTGAA TGAAGCCACA GGTACAAAGA TTGCTTATGA AACAAAAGTG GACTTGGTCC AAACATCAGA AGCTATACAA GAATCACTTT ACCCCACAGC
   S  E  L  N  E  A  T  G  T  K  I  A  Y  E  T  K  V  D  L  V  Q  T  S  E  A  I  Q  E  S  L  Y  P  T  570

ACAGCTTTGC CCATCATTTG AGGAAGCTGA AGCAACTCCG TCACCAGTTT TGCCTGATAT TGTTATGGAA GCACCATTAA ATTCTCTCCT TCCAAGCGCT
A  Q  L  C  P  S  F  E  E  A  E  A  T  P  S  P  V  L  P  D  I  V  M  E  A  P  L  N  S  L  L  P  S  A  604
```

FIG.2A2

GGTGCTTCTG TAGTGCAGCC CAGTGTATCC CCACTGGAAG CACCTCCTCC AGTTAGTTAT GACAGTATAA AGCTTGAGCC TGAAAACCCC CCACCATATG
G A S V V Q P S V S P L E A P P P V S Y D [S] I K L E P E N P P P Y 637

AAGAAGCCAT GAATGTAGCA CTAAAAGCTT TGGGAACAAA GGAAGGAATA AAAGAGCCTG AAAGTTTTAA TGCAGCTGTT CAGGAAACAG AAGCTCCTTA
E E A M N V A L K A L G T K E G I K E P E S F N A A V Q E T E A P 670

TATATCCATT GCGTGTGATT TAATTAAAGA AACAAAGCTC TCCACTGAGC CAAGTCCAGA TTTCTCTAAT TATTCAGAAA TAGCAAAATT CGAGAAGTCG
Y I S I A C D L I K E T K L S T E P S P D F S N Y S E I A K F E K S 704

GTGCCCGAAC ACGCTGAGCT AGTGGAGGAT TCCTCACCTG AATCTGAACC AGTTGACTTA TTTAGTGATG ATTCGATTCC TGAAGTCCCA CAAACACAAG
V P E H A E L V E D S S P E S E P V D L F S D D S I P E V P Q T Q 737

AGGAGGCTGT GATGCTCATG AAGGAGAGTC TCACTGAAGT GTCTGAGACA GTAGCCCAGC ACAAAGAGGA GAGACTTAGT GCCTCACCTC AGGAGCTAGG
E E A V M L M K E S L T E V S E T V A Q H K E E R L S A S P Q E L 770

AAAGCCATAT TTAGAGTCTT TTCAGCCCAA TTTACATAGT ACAAAAGATG CTGCATCTAA TGACATTCCA ACATTGACCA AAAAGGAGAA AATTTCTTTG
G K P Y L E S F Q P N L H [S] T K D A A S N D I P T L T K K E K I S L 804

CAAATGGAAG AGTTTAATAC TGCAATTTAT TCAAATGATG ACTTACTTTC TTCTAAGGAA GACAAAATAA AAGAAAGTGA AACATTTTCA GATTCATCTC
Q M E E F N T A I Y S N D D L L [S] S K E D K I K E S E T F S D S S 837

CGATTGAGAT AATAGATGAA TTTCCCACGT TTGTCAGTGC TAAAGATGAT TCTCCTAAAT TAGCCAAGGA GTACACTGAT CTAGAAGTAT CCGACAAAAG
P I E I I D E F P T F V [S] A K D D [S] P K L A K E Y T D L E V [S] D K 870

TGAAATTGCT AATATCCAAA GCGGGGCAGA TTCATTGCCT TGCTTAGAAT TGCCCTGTGA CCTTTCTTTC AAGAATATAT ATCCTAAAGA TGAAGTACAT
S E I A N I Q S G A D S L P C L E L P C D L [S] F K N I Y P K D E V H 904

GTTTCAGATG AATTCTCCGA AAATAGGTCC AGTGTATCTA AGGCATCCAT ATCGCCTTCA AATGTCTCTG CTTTGGAACC TCAGACAGAA ATGGGCAGCA
V S D E F S E N R S S V S K A S I S P S N V S A L E P Q T E M G S 937

FIG.2A3

```
TAGTTAAATC CAAATCACTT ACGAAAGAAG CAGAGAAAAA ACTTCCTTCT GACACAGAGA AAGAGGACAG ATCCCTGTCA GCTGTATTGT CAGCAGAGCT
 I  V  K  S  K  S  L  T  K  E  A  E  K  K  L  P  S  D  T  E  K  E  D  R  S  L  S  A  V  L  S  A  E   970

GAGTAAAACT TCAGTTGTTG ACCTCCTCTA CTGGAGAGAC ATTAAGAAGA CTGGAGTGGT GTTTGGTGCC AGCTTATTCC TGCTGCTGTC TCTGACAGTG
 L  S  K  T  S  V  V  D  L  L  Y  W  R  D  I  K  K  T  G  V  V  F  G  A  S  L  F  L  L  L  S  L  T  V  1004

TTCAGCATTG TCAGTGTAAC GGCCTACATT GCCTTGGCCC TGCTCTCGGT GACTATCAGC TTTAGGATAT ATAAGGGCGT GATCCAGGCT ATCCAGAAAT
 F  S  I  V  S  V  T  A  Y  I  A  L  A  L  L  S  V  T  I  S  F  R  I  Y  K  G  V  I  Q  A  I  Q  K  1037

CAGATGAAGG CCACCCATTC AGGGCATATT TAGAATCTGA AGTTGCTATA TCAGAGGAAT TGGTTCAGAA ATACAGTAAT TCTGCTCTTG GTCATGTGAA
 S  D  E  G  H  P  F  R  A  Y  L  E  S  E  V  A  I  S  E  E  L  V  Q  K  Y  S  N  S  A  L  G  H  V  1070

CAGCACAATA AAAGAACTGA GGCGGCTTTT CTTAGTTGAT GATTTAGTTG ATTCCCTGAA GTTTGCAGTG TTGATGTGGG TGTTTACTTA TGTTGGTGCC
 N  S  T  I  K  E  L  R  R  L  F  L  V  D  D  L  V  D  S  L  K  F  A  V  L  M  W  V  F  T  Y  V  G  A  1104

TTGTTCAATG GTCTGACACT ACTGATTTTA GCTCTGATCT CACTCTTCAG TATTCCTGTT ATTTATGAAC GGCATCAGGT GCAGATAGAT CATTATCTAG
 L  F  N  G  L  T  L  L  I  L  A  L  I  S  L  F  S  I  P  V  I  Y  E  R  H  Q  V  Q  I  D  H  Y  L  1137

GACTTGCAAA CAAGAGTGTT AAGGATGCCA TGGCCAAAAT CCAAGCAAAA ATCCCTGGAT TGAAGCGCAA AGCAGATTGA AAAAGCCCCA AACAGAAGTT
 G  L  A  N  K  S  V  K  D  A  M  A  K  I  Q  A  K  I  P  G  L  K  R  K  A  D  *                    1163

CATCTTTAAA GGGGACACTC ACTTGATTAC GGGGGTGGGA GGGTCAGGGG TGAGCCCTTG GTGGCCGTGC GGTTTCAGCT CTTTATTTTT AGCAGTGCAC
TGTTTGAGGA AAAATTACCT GTCTTGACTT CCTGTGTTTA TCATCTTAAG TATTGTAAGC TGCTGTGTAT GGATCTCATT GTAGTCACAC TTGTCTTCCC
CAATGAGGCG CCTGGTGAAT AAAGGACTCG GGGAAAGCTG TGCATTGTAT CTGCTGCAGG GTAGTCTAGC TGTATGCAGA GAGTTGTAAA GAAGGCAAAT
CTGGGGGCAG GGAAAACCCT TTTCACAGTG TACTGTGTTT GGTCAGTGTA AAACTGATGC AGATTTTTCT GAAATGAAAT GTTTAGATGA GAGCATACTA
CTAAAGCAGA GTGGAAAACT CTGTCTTTAT GGTGTGTTCT AGGTGTATTG TGAATTTACT GTTATATTGC CAATATAAGT AAATATAGAC CTAATCTATA
TATAGTGTTT CACAAAGCTT AGATCTTTAA CCTTGCAGCT GCCCCACAGT GCTTGACCTC TGAGTCATTG GTTATGCAGT GTAGTCCCAA GCACATAAAC
TAGGAAGAGA AATGTATTTG TAGGAGTGCT ACCTACCACC TGTTTTCAAG AAAATATAGA ACTCCAACAA AAATATAGAA TGTCATTTCA AAGACTTACT
GTATGTATAG TTAATTTTGT CACAGACTCT GAAATTCTAT GGACTGAATT TCATGCTTCC AAATGTTTGC AGTTATCAAA CATTGTTATG CAAGAAATCA
TAAAATGAAG ACTTATACCA TTGTGGTTTA AGCCGTACTG AATTATCTGT GGAATGCATT GTGAACTGTA AAAGCAAAGT ATCAATAAAG CTTATAGACT
TAAAAAAAAA AAAAAAAAAA
```

FIG. 2A4

peptide 1:	EYLGDLPAVLPTE	peptide 4:	KXFEXVWEV
(bovine)	EYLGDLPAVLPTE	(bovine)	KPFERVWEV
(rat)	gYLGnLsAVsssE	(rat)	KPFEQaWEV
peptide 2:	EIAEIQDG ESL	peptide 5:	VVDLLYWRDIK
(bovine)	EIAdIQDGagSL	(bovine)	VVDLLYWRDIK
(rat)	EIAnIQsGadSL	(rat)	VVDLLYWRDIK
peptide 3:	KXYLESIQPSLGITK	peptide 6:	KAVAAEASMREEYADF
(bovine)	KPYLESfQPSLGITK	(bovine)	KgVAAEASMgEEYADF
(rat)	KPYLESfQPnLhsTK	(rat)	mqmsvvApvREEYADF

FIG.2B

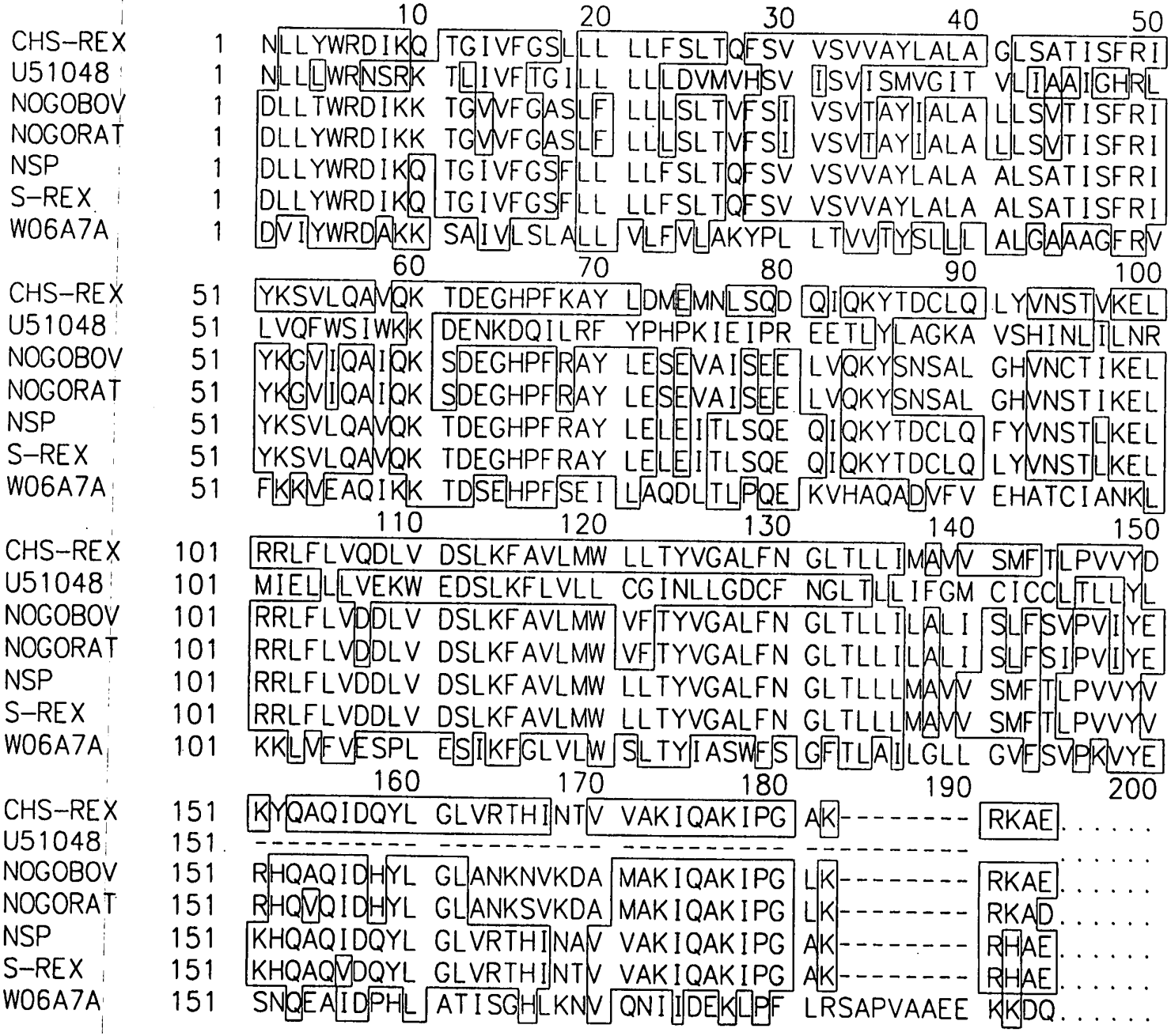


FIG. 3A

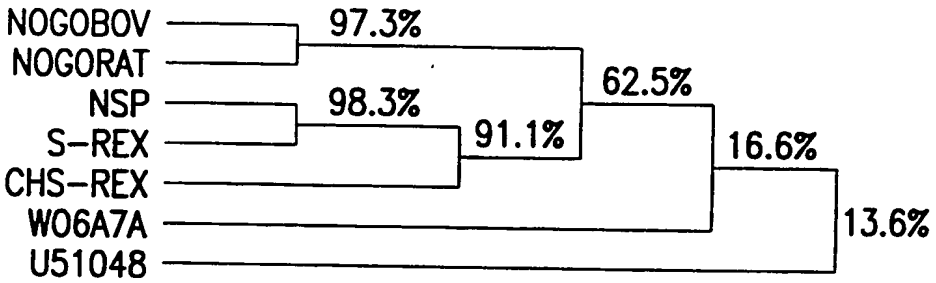

NOGOBOV
NOGORAT
NSP
S-REX
CHS-REX
W06A7A
U51048
97.3%
98.3%
91.1%
62.5%
16.6%
13.6%

FIG. 3B

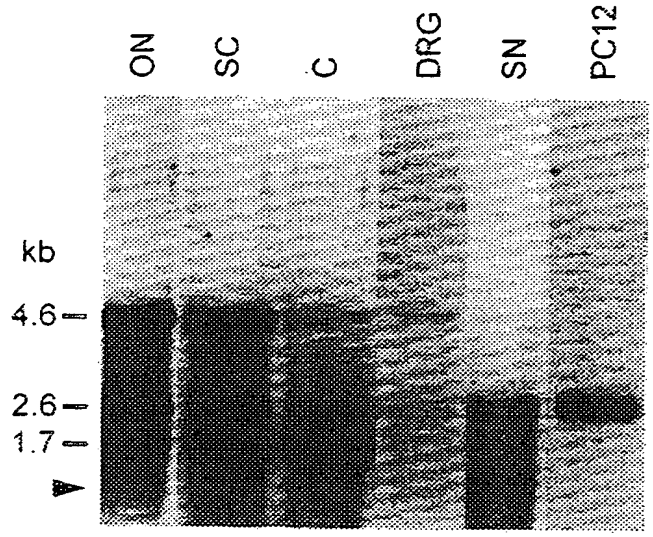


FIG.4A

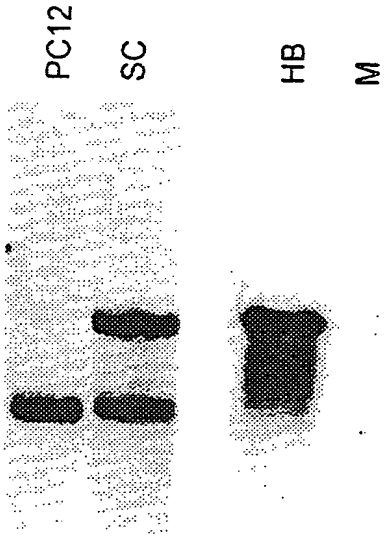


FIG.4B

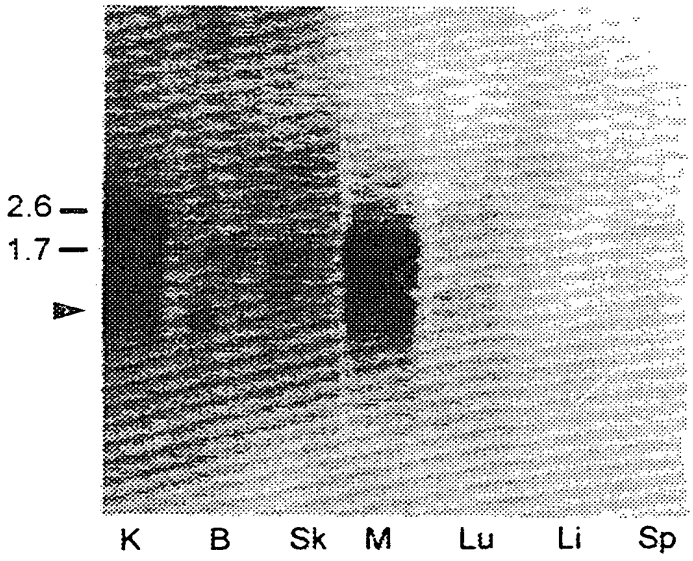


FIG.4C

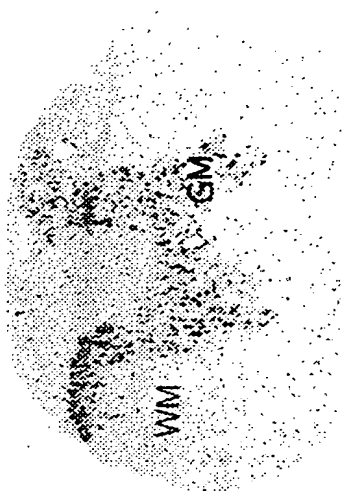


FIG.5C

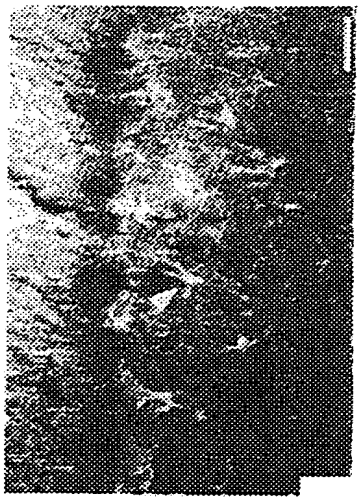


FIG.5F

FIG.5B

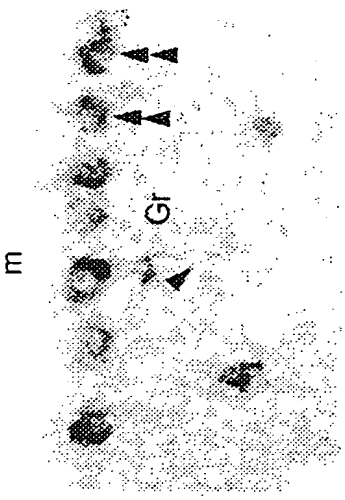


FIG.5E

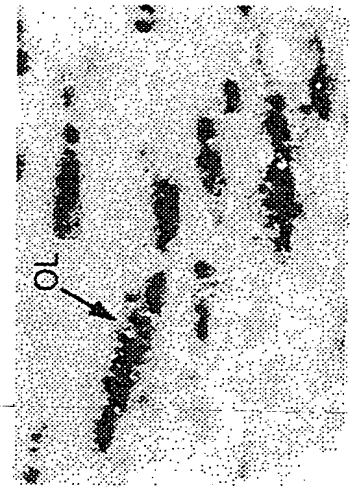


FIG.5A

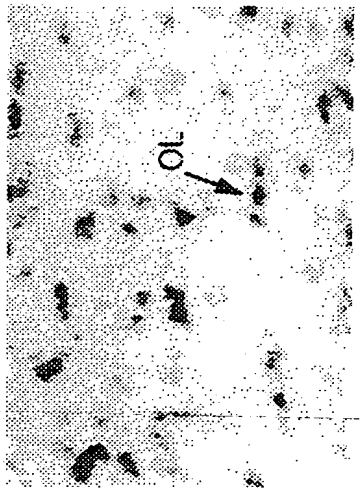


FIG.5D

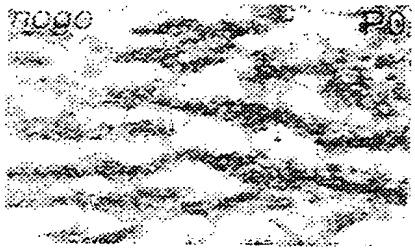


FIG.6A

FIG.6B

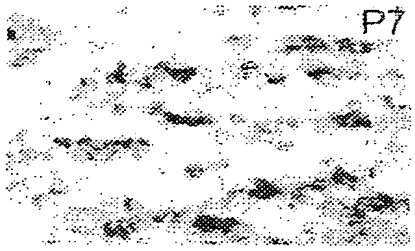


FIG.6C

FIG.6D

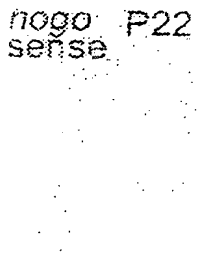


FIG.6E

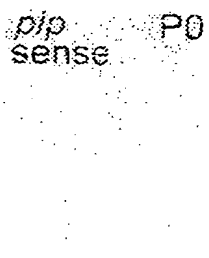


FIG.6F

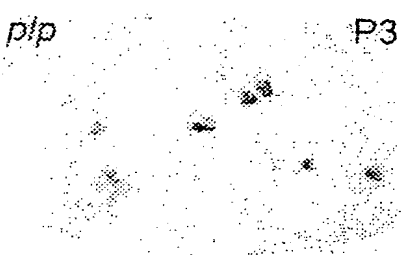


FIG.6G

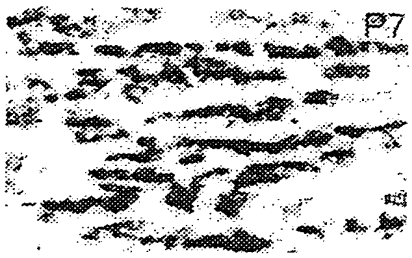


FIG.6H

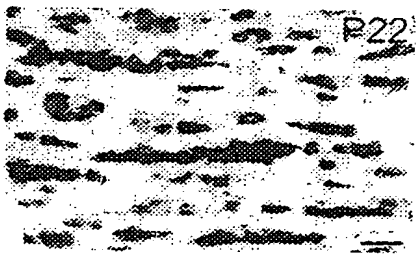


FIG.6I

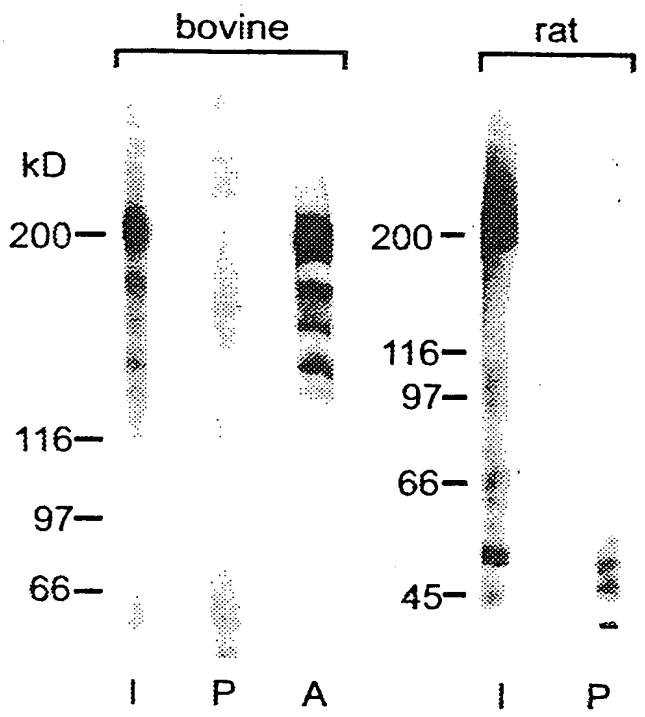


FIG.7A FIG.7B

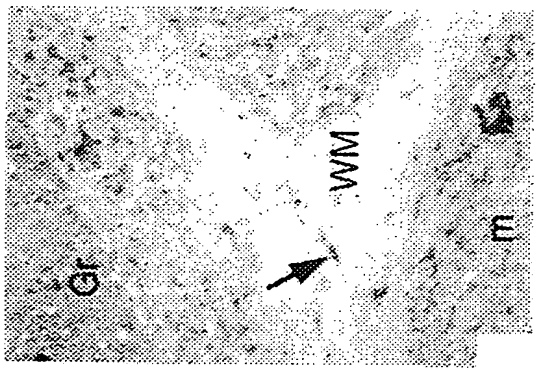


FIG.8C

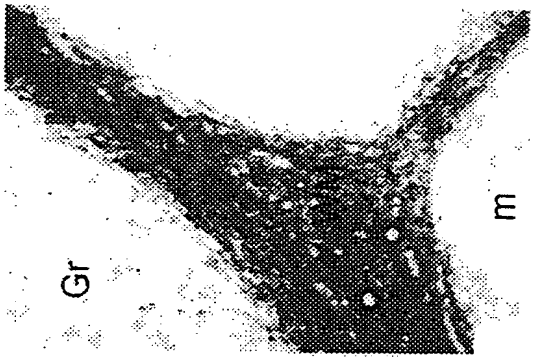


FIG.8B

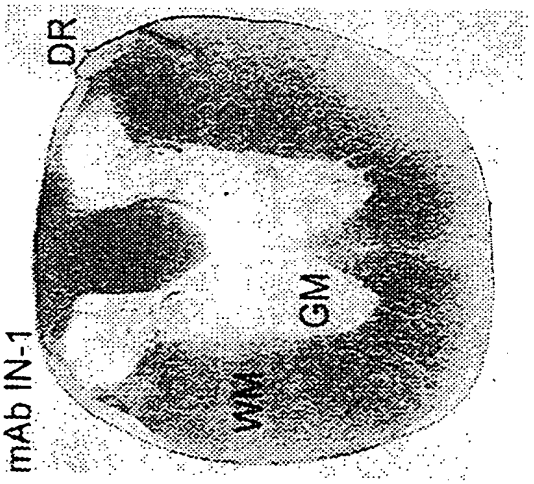


FIG.8A

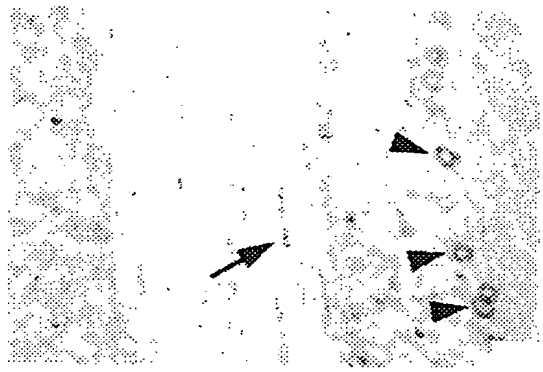


FIG.8F

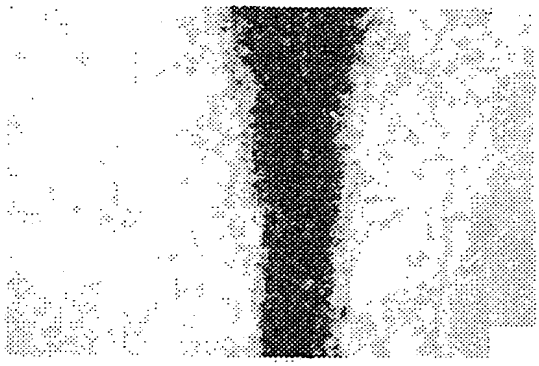


FIG.8E

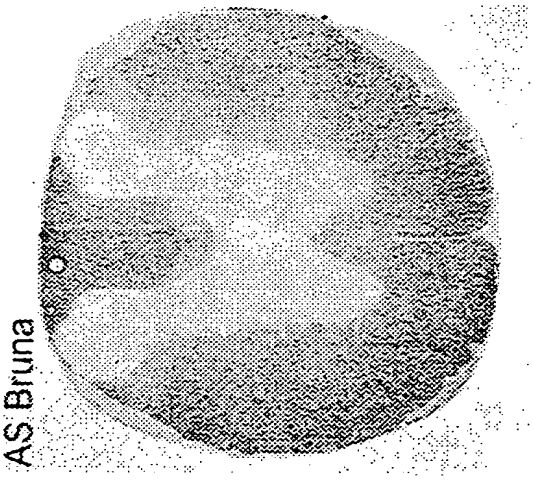


FIG.8D

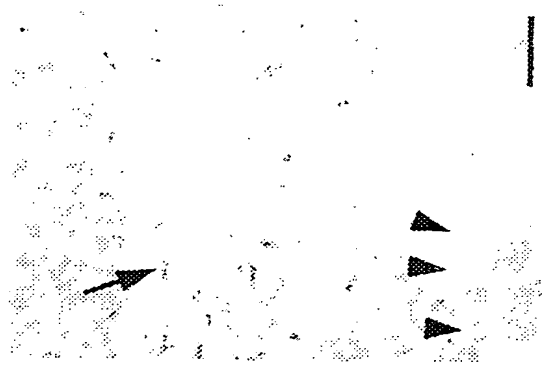


FIG.8I

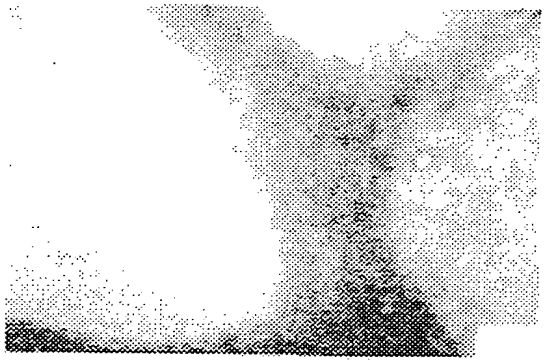


FIG.8H

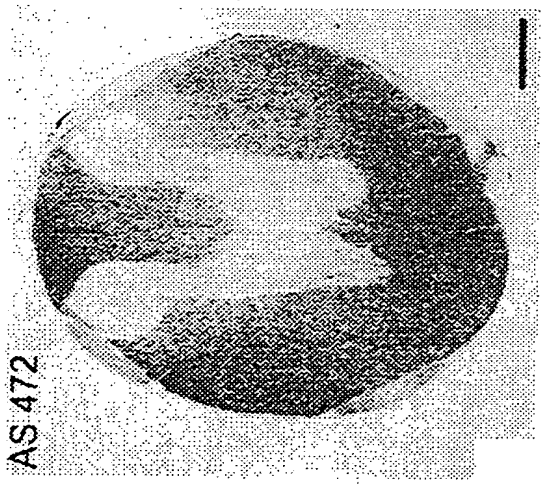


FIG.8G

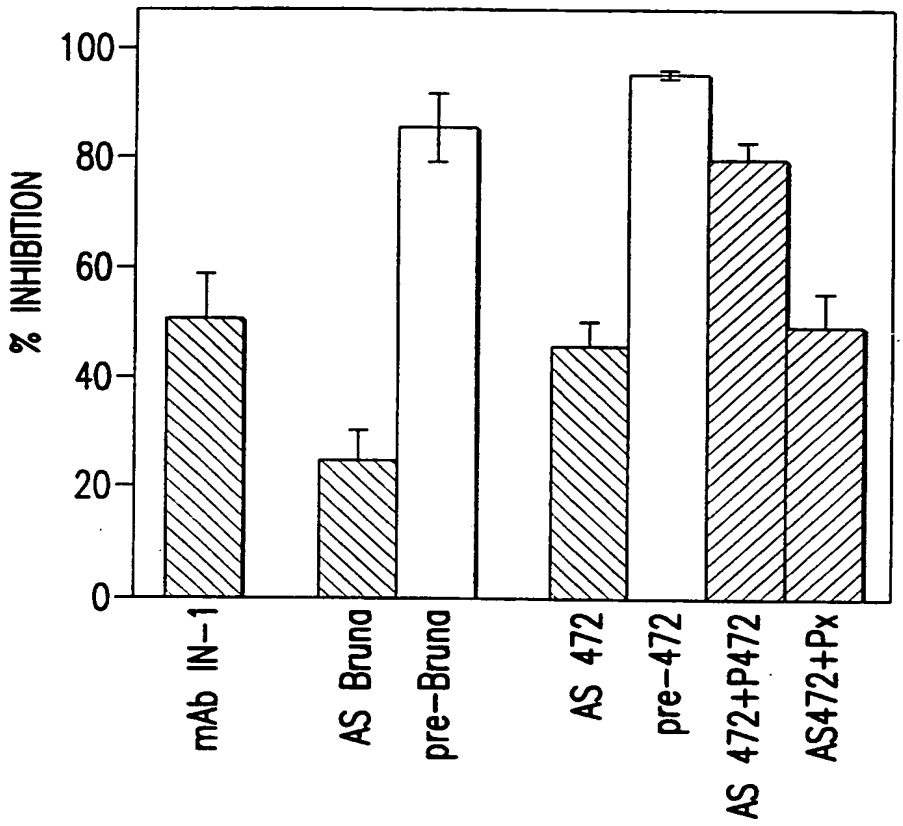

% INHIBITION
100
80
60
40
20
0
mAb IN-1
AS Bruna
pre-Bruna
AS 472
pre-472
AS 472+P472
AS472+Px

FIG.9A

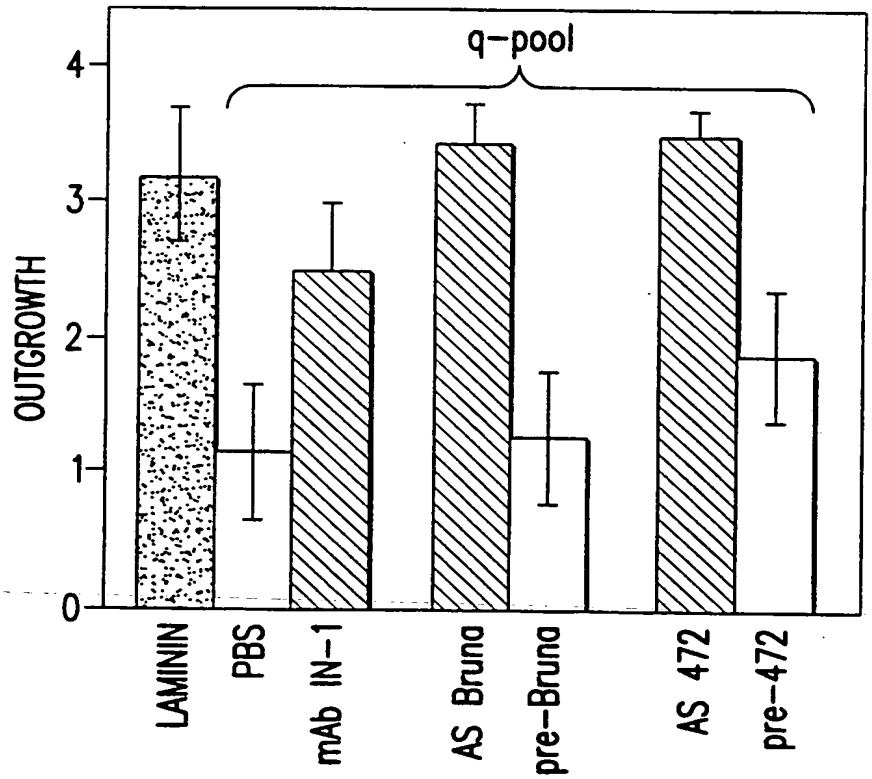

q-pool
OUTGROWTH
4
3
2
1
0
LAMININ
PBS
mAb IN-1
AS Bruna
pre-Bruna
AS 472
pre-472

FIG.9B

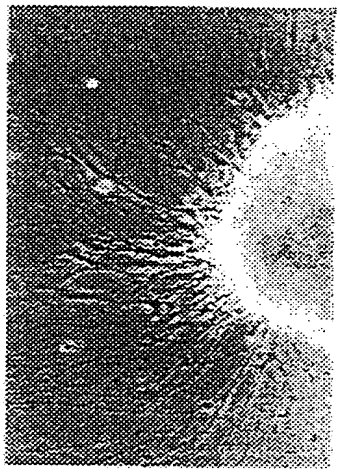


FIG.9D

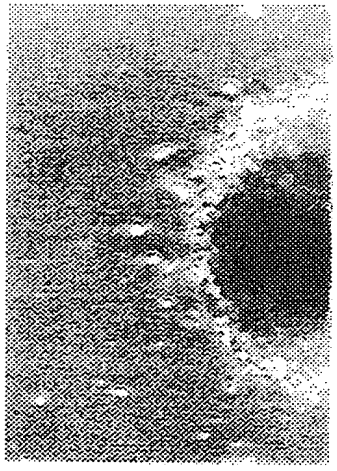


FIG.9C

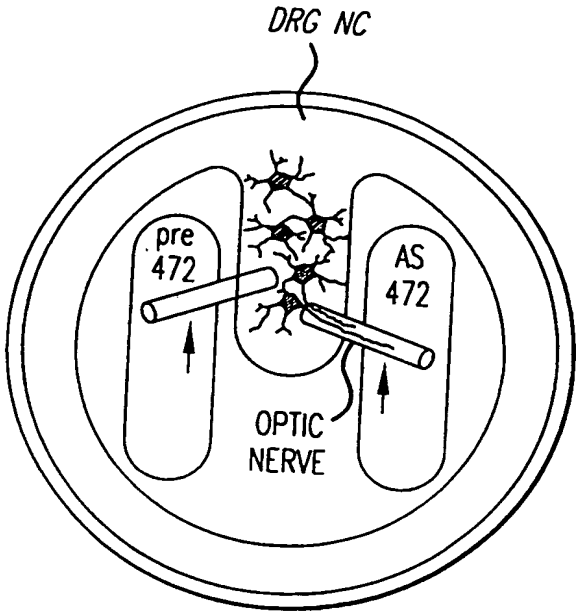


FIG. 10A

CULTURE	pre–472	AS 472
1	–	++
2	–	+++
3	+	+++
4	+	–
5	–	+++
6	+	+++
7	++	++
8	+	++
9	+	++
10	–	+++

AXONS/NERVE:–=0;+=1–20;++=20–50;+++=50–>300

FIG. 10B

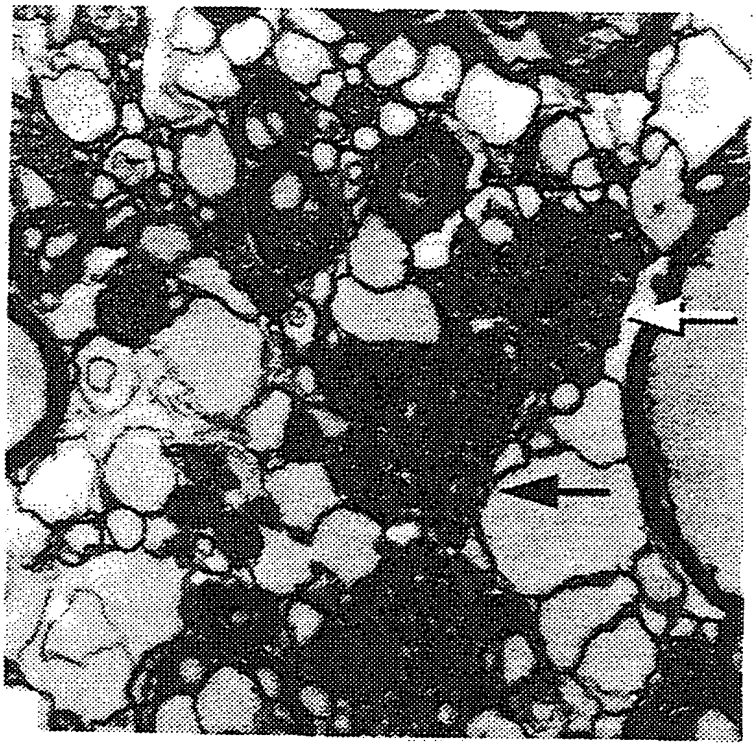


FIG. 10C

FIG. 10D

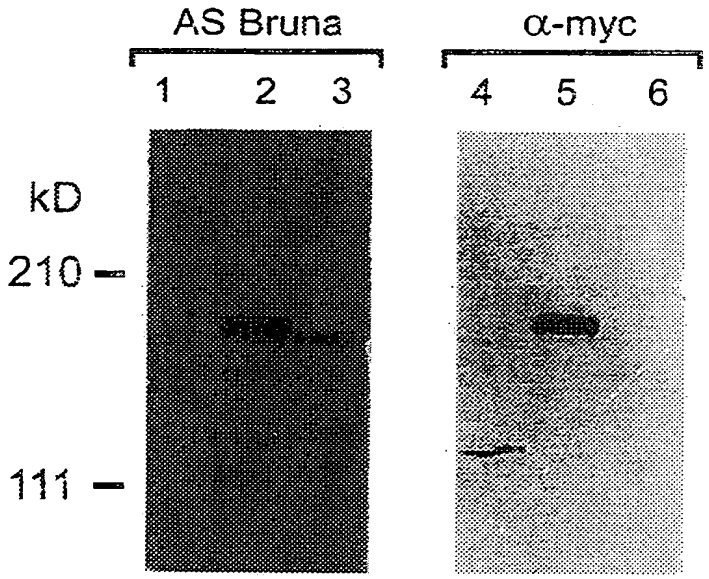


FIG. 11A

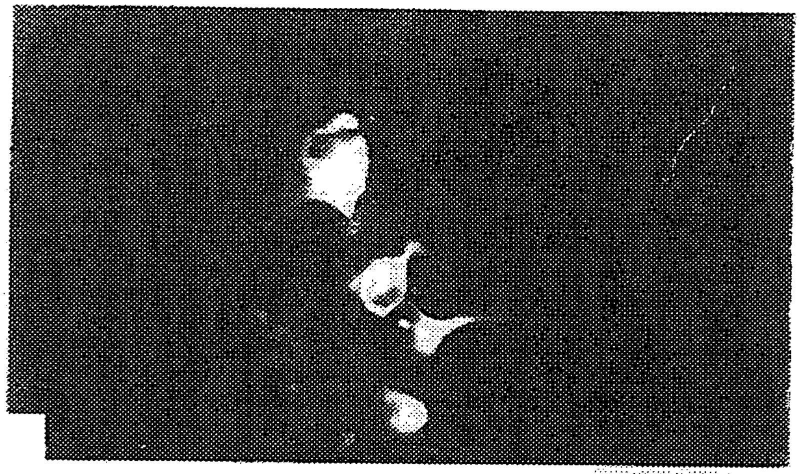


FIG.11B

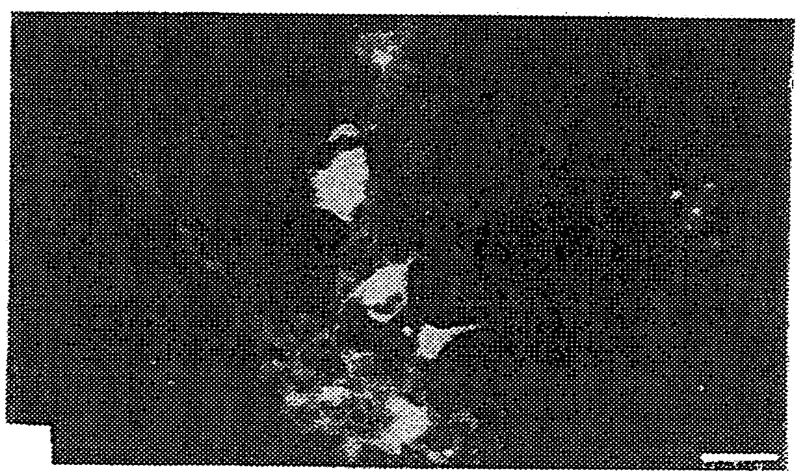


FIG.11C

```
        10         20         30         40         50         60
CTATCTCCTC TCTCAGCCGC TGCTTTTAAA GAACGTGAAT ACCTTGGTGA TTTACCAGCA
        70         80         90        100        110        120
GTACTGCCCA CTGAAGGAAC ACTTCCAGCA ACTTCAAATG AAGCTTCTAA AGCATTCTCA
       130        140        150        160        170        180
GAGAAGGCAA AAAATCCATT TGTAGAGAGA AATTTAACAG AATTTTCAGA ATTGGAATAT
       190        200        210        220        230        240
TCAGAAATGG AATCATCATT CAGTGGCTCT CAAAAGGCAG AACCTGCCGT AACAGTAGCG
       250        260        270        280        290        300
AATCCTAGGG ACGAAATAGT TGTGAGGAGT AGAGATAAAG AAGAGGACTT AGTTAGTCTT
       310        320        330        340        350        360
AACATCCTTC ATACTCAGCA GGAGTTATCT ACAGTCCTTA CGAAATCAGT TGAAGAAGAA
       370        380        390        400        410        420
GATAGAGTTC TGTCTCCAGA AAAAACAAAG GACAGTTTTA AGGAAAAGGG AGTTGCAGCA
       430        440        450        460        470        480
GAAGCTTCTA TGGGGGAGGA ATATGCAGAC TTCAAACCAT TTGAGCGAGT ATGGGAAGTG
       490        500        510        520        530        540
AAAGATACTT ACAAGCAAGA TAGTGATGTT TTGATTGCTG GAGGTAATAT AGAGAGCAAA
       550        560        570        580        590        600
TTGGAAGGTA AAGTGGATAA GAAACACTTT TCAGATAGCC TTGAACAAAC AAATCGTGAA
       610        620        630        640        650        660
AAAGATAGTG AAAGCAGTAA TGATGACACT TCATTTCCCA GTACACCAGA AGCTGTAAGA
       670        680        690        700        710        720
GGTGGTTCCG GAGCGTACAT CACGTGTGCT CCCTTTAACC CAACAACTGA GAATGTTTCA
       730        740        750        760        770        780
ACAAACATTT TTCCCTTGTT GGAAGATCAT ACTTCGGAAA ATAAGACAGA TGAAAAAAAG
       790        800        810        820        830        840
ATAGAAAAAA AAAGGCACAA ATTGTAACAG AGAAGAATGC AAGTGTCAAG ACATCAAACC
       850        860        870        880        890        900
CTTTCCTTAT GGCAGCACAG GAGTCTAAGA CAGATTACGT TACAACAGAT CATGTGTCAA
       910        920        930        940        950        960
AGGTGACCGA GGAAGTAGTG GCAAACATGC CTGAAGGTCT AACCCCAGAT TTGGTTCAGG
       970        980        990       1000       1010       1020
AAGCATGTGA AAGTGAATTG AATGAAGCTA CTGGTACAAA AATTGCCTTT GAAACAAAAA
      1030       1040       1050       1060       1070       1080
TGGACCTGGT TCAAACTTCA GAAGCTGTGC AGGAGTCACT TTACCCTGTA ACACAGCTTT
      1090       1100       1110       1120       1130       1140
GCCCATCTTT TGAAGAATCT GAAGCTACTC CGTCACCGGT TTTGCCTGAC ATTGTCATGG
      1150       1160       1170       1180       1190       1200
AAGCACCATT AAATTCTGTA GTTCCTAGTG CTGGTGCTTC TGCAGTGCAG CTCAGTTCAT
      1210       1220       1230       1240       1250       1260
```

FIG 12A

CACCATTAGA AACTCTTCCT TCAGTTAATT ATGAAAGCAT AAAGTTTGAG CCTGAAAATC
1270 1280 1290 1300 1310 1320
CCCCACCATA TGAGGAGGCC ATGAATGTAT CACTAAAAAA AGAATCAGGA ATGAATGAAG
1330 1340 1350 1360 1370 1380
AAATCACAGA GCCTGAAGGT ATTAGTGTAG CTGTTCAGGA AACAGAAGCT CCTTATATAT
1390 1400 1410 1420 1430 1440
CTATTGCATG TGATTTAATT AAAGAAACAA AGATCTCTAC TGAACCGACT CCAGATTTCT
1450 1460 1470 1480 1490 1500
CTAGTTATTC AGAAATAGCA GAAGTTGCAC AGCCAGTGCC CGAGCATTCT GAGCTAGTTG
1510 1520 1530 1540 1550 1560
AAGATTCCTC CCCCGATTCT GAACCAGTTG ACTTATTTAG TGATGATTCA ATACCCGAAG
1570 1580 1590 1600 1610 1620
TTCCACAAAA ACAAGATGAA GCTGTAATAC TTGTGAAAGA AAACCTCACT GAAATTTCAT
1630 1640 1650 1660 1670 1680
CTGAGTCAAT GACAGGACAT GACAATAAGG GAAAACTCAG TGCTTCACCA TCACCTGAGG
1690 1700 1710 1720 1730 1740
GAGGAAAACC GTATTTGGAG TCTTTTCAGC CCAGTTTAGG CATCACAAAA GATACCTTAG
1750 1760 1770 1780 1790 1800
CACCTGATGA AGTTTCAGCA TTGACCCAAA AGGAGAAAAT CCCTTTGCAG ATGGAGGAGC
1810 1820 1830 1840 1850 1860
TCAATACTGC AGTTTATTCA AGTGATGGCT TATTCATTGC TCAGGAAGCA AACCTAAGAG
1870 1880 1890 1900 1910 1920
AAAGTGAAAC ATTTTCAGAT TCATCTCCGA TTGAGATTAT AGATGAGTTC CCGACCTTTG
1930 1940 1950 1960 1970 1980
TCAGTTCTAA AGCAGATTCT TCTCCTACAT TAGCCAGGGA ATACACTGAC CTAGAAGTAG
1990 2000 2010 2020 2030 2040
CCCACAAAAG TGAAATTGCT GACATCCAGG ATGGAGCTGG GTCATTGGCT TGTGCAGGAT
2050 2060 2070 2080 2090 2100
TGCCCCATGA CCTTTCTTTC AAGAGTATAC AACCTAAAGA GGAAGTTCAT GTCCCAGATG
2110 2120 2130 2140 2150 2160
AGTTCTCCAA AGATAGGGGT GATGTTTCAA AGGTGCCCGT ACTGCCTCCA GATGTTTCTG
2170 2180 2190 2200 2210 2220
CTTTGGATGC TCAAGCAGAG ATAGGCAGCA TAGAAAAACC CAAAGTTCTT GTGAAAGAAG
2230 2240 2250 2260 2270 2280
CCGAGAGAAA ACTTCCTTCT GATACAGAAA AAGAGCGAAG ATCTCCATCT GCTATATTTT
2290 2300 2310 2320 2330 2340
CAGCAGAGCT GAGTAAAACT TCAGTTGTTG ACCTCCTCTA CTGGAGAGAC ATTAAGAAGA
2350 2360 2370 2380 2390 2400
CTGGAGTGGT GTTTGGTGCC AGCTTGTTCC TGCTGCTCTC GCTGACAGTA TTCAGCATTG
2410 2420 2430 2440 2450 2460

FIG. 12B

TGAGTGTAAC GGCCTACATT GCCTTGGCCC TGCTCTCTGT GACTATCAGC TTTAGGATAT
2470 2480 2490 2500 2510 2520
ATAAGGGTGT GATCCAGGCT ATCCAGAAAT CTGATGAAGG CCACCCATTC AGGGCATATT
2530 2540 2550 2560 2570 2580
TGGAATCTGA AGTTGCTATA TCTGAGGAGT TGGTTCAGAA GTACAGCAAT TCTGCTCTTG
2590 2600 2610 2620 2630 2640
GTCATGTTAA CTGCACAATA AAAGAACTCA GACGCCTCTT CTTAGTTGAT GATTTAGTTG
2650 2660 2670 2680 2690 2700
ATTCTCTGAA GTTTGCAGTG TTGATGTGGG TATTTACCTA TGTTGGTGCC TTGTTCAATG
2710 2720 2730 2740 2750 2760
GTCTGACACT ACTAATTTTG GCTCTGATTT CACTCTTCAG TGTTCCTGTT ATTTATGAAC
2770 2780 2790 2800 2810 2820
GGCATCAGGC GCAAATAGAT CATTATCTGG GACTTGCAAA TAAGAATGTT AAAGATGCTA
2830 2840 2850 2860 2870 2880
TGGCTAAAAT CCAAGCAAAA ATCCCTGGAT TGAAGCGTAA AGCTGAATGA GAAAGCCTGA
2890 2900 2910 2920 2930 2940
AAGAGTTAAC AATAGAGGAG TTTATCTTTA AAGGGGATAT TCATTTGATT CCATTGGGGA
2950 2960 2970 2980 2990 3000
GGGTCAGGGA AGAACAAAGC CTTGACATTG CAGTGCAGTT TCACAGATCT TTATTTTTAG
3010 3020 3030 3040 3050 3060
CAACGCAGTG TCTGAGGAAA AATGACCTGT CTTGACTGCC CTGTGTTCAT CATCTTAAGT
3070 3080 3090 3100 3110 3120
ATTGTAAGCT GCTATGTATG GATTTAAATC GTAATCATAT TTGTTTTTCC TGTATGAGGC
3130 3140 3150 3160 3170 3180
ACTGGTGAAT AAACAAAGAT CTGAGAAAGC TGTATATTAC ACTTTGTCGC AGGTAGTCTT
3190 3200 3210 3220 3230 3240
GCTGTATTTG GGGAATTGCA AAGAAAGTGG AGCTGACAGA AATAACCCTT TTCACAGTTT
3250 3260 3270 3280 3290 3300
GTGCACTGTG TACGGTCTGT GTAGGTTGAT GCAGATTTTC TGAAATGAAA TGTTTAGACG
3310 3320 3330 3340 3350 3360
AGATCATGCC ACCAAGGCAG GAGTGAAAAA GCTTGCCTTT CCTGGTATGT TCTAGGTGTA
3370 3380 3390 3400 3410 3420
TTGTGAAATT TACTGTTGTA TTAATTGCCA ATATAAGTAA ATATAGATTA TATATATCTA
3430 3440 3450 3460 3470 3480
TATATAGTGT TTCACGAAGC TTAGCCCTTT ACCTTCCCAG CTGCCCCACA GTGCTTGATA
3490 3500 3510 3520 3530 3540
CTTCTGTCAT GGGTTTTATG TGTGTAGTCC CAAAGCACAT AAGCTAGGGA GAAACGTACT
3550 3560 3570 3580 3590 3600
TCTAGGCGCA CTACCATCTG TTTTCAACAC GAACCGACGC CATGCAAACA GAACTCCTCA
3610 3620 3630 3640 3650 3660
ACATAAACTT CACTGCACAG ACTTACTGTA GTTAATTTTA TCACAAACTC TGGACTGAAT
3670 3680 3690 3700 3710 3720

FIG. 12C

```
CTAATGCTTC CAAAAATGTT TGCAAATATC AAACATTGTT ATGTAAGAAA ATATAAATGA
      3730       3740       3750       3760       3770       3780
CGATTTATAC AATTGTGGTT TAAGCTGTAT TGAACTAAAT CTGTGGAATG CATTGTGAAC
      3790       3800       3810       3820       3830       3840
TGTAAAAGCA AAGTATCAAT AAAGCTTATA GACTTAAAAA AAAAAAAAAA AAA.......
```

FIG. 12D

```
1   MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEE-EEEDEDE   50
    ||| ||| ||||| |||||| |||||||| |||||| ||||| |||| ||
1   MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEED-DE   50

51  DLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAA   100
    |||||||||||||||||| || | || ||| || | ||||||||||||
51  DLEELEVLERKPAAGLSAAAVPPA-AA-APLLDFSSDSVPPAPRGPLPAA   100

101 PPVAPERQPSWDPSPVSSTVPAPSPLS-AAAVSPSKLPEDDEPPARPPPP  150
    || |||||||| ||      |||| |  |||| ||||||||||||||||||
101 PPAAPERQPSWERSPAA---PAPS-LPPAAAVLPSKLPEDDEPPARPPPP  150

151 PPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGS-SG-----AV-----  200
    |||  || |||     | ||  | ||||||||||| |       |
151 PPAGASPLAEP-----A-AP--P-STPAAPKRRGSGSVDETLFALPAASE  200

201 -VXXXX--KIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASF  250
    |||||  ||||| |||||| | ||||||||||||||||||||||||  ||
201 PVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASXPSLSPLSTVSF  250

251 KEHEYLGNLSTVLPTEGTLQE--NVSEASKEVSEKAKTLLID-RDLTEFS  300
    ||| |||||| |   ||| |  | |||||  | | |     ||| |||
251 KEHGYLGNLSAVSSSEGTIEETLN--EASKELPERA-TNPFVNRDLAEFS  300

301 ELEYSEMGSSFSVSPKAESAVI-VANPREEIIVKNKDEEEKLV-SNNILH  350
    |||||||||||  ||| ||| | | |  || ||  || |  || |   ||
301 ELEYSEMGSSFKGSPKGESA-ILVENTKEEVIVRSKDKED-LVCSAA-LH  350

351 XQQELPTALTKLV-KEDEVVSSEKAKDSFNEKR--VAVEAPMREEYADFK  400
    | || |      | ||| ||| ||  | |||    | | || ||||||||
351 SPQESP------VGKEDRVVSPEKTMDIFNEMQMSV-V-APVREEYADFK  400

401 PFERVWEVKDSKEDS-DMLAAGGKIESNLESKVDKKCFADSLEQTNHEKD  450
    |||  |||||  | | | |||      | |||||  ||  |||||    ||
401 PFEQAWEVKDTYEGSRDVLAARA----NVESKVDRKCLEDSLEQKSLGKD  450

451 SESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT-NIFPLLEDP  500
    ||  | | |||||||  || | |||||| |  | |||  | | |||||||
451 SEGRNEDASFPSTPEPVKDSSRAYITCASFTSA-TEST-TANTFPLLEDH  500

501 TSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLT  550
    |||||||||||||| |||| ||| || |||||| || |||| |||||| |
501 TSENXTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS  550

551 KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVM  600
    ||||  | ||||||||||||||||||||| |||||||||| |||||||
551 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAI  600
```

FIG. 13A

```
601  QESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSS  650
     ||||||  |||||||||  ||||||||||||||||||||  |||||||  |||
601  QESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSV  650

651  SPLEASS-VNYESIKHEPENPPPYEEAMSVSLKVSGIKEEIKEPENINAA  700
     |||||   | | |||  ||||||||||||  | ||  | ||  |||||  |||
651  SPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESFMAA  700

701  LQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVE  750
     ||||||||||||||||||||  || ||||  |||  ||  |   ||  ||||
701  VQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVE  750

751  DSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMIEYENKE  800
     ||||  ||||||||||||||  |||  |  |  |||  ||||||  |  |          ||
751  DSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS-ETVAQH--KE  800

801  K-LSALPPEGGKPYLESFK--L-SLDNTKDTLLPDEVSTLSKKEKIPLQM  850
       |||  |  |  ||||||||    |  |   |||     |    ||  ||||||  |||
801  ERLSASPQELGKPYLESFQPNLHS---TKDAASNDIP-TLTKKEKISLQM  850

851  EELSTAVYSNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTDSF  900
     ||   ||  ||||||   |||   |  |  ||||||||||||||||||   |  |  ||
851  EEFNTAIYSNDDLSSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDSP  900

901  SKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKI  950
       |||  ||||||||  ||||||    ||  ||||  |||  |||  |||  ||  |
901  -KLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPKDEVHV  950

951  SFSDDFSKNGSATSKVLLLPPDVSALGHTQAEIESIVKPKVLEKEAEKKL  1000
     |  |  ||  |  |  ||     |  ||||   |  |  ||||  |  |  |||||||
951  S--DEFSENRSSVSKASISPSNVSALEP-QTEMGSIVKSKSLTKEAEKKL  1000

1001 PSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSL  1050
     ||||||||||  ||  ||  |  ||||||||||||||||||||||||||||||
1001 PSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSL  1050

1051 TVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEV  1100
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
1051 TVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEV  1100

1101 AISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYV  1150
     ||||||||||||||||||  ||||||||||||||||||||||||||||||
1101 AISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYV  1150

1151 GALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQ  1200
     ||||||||||||||||||  ||||||||  ||||||||||  |||||||||
1151 GALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQ  1200

1201 AKIPGLKRKAE.....                                   1250
     ||||||||||
1201 AKIPGLKRKAD.....                                   1250
```

FIG. 13B

```
1   CAG GCT TAG TCT GGG GAA GCG GGT GTT TCA TGT CTC AGG GAG
      Q   A   -   S   G   E   A   G   V   S   C   L   R   E

43  AAT TTT GCA GTT TAC AGC GTT TCT GTT GGT ATG CAT AAT TTG
      N   F   A   V   Y   S   V   S   V   G   M   H   N   L

                                                START
85  TAA TTG CTG CTG GAG GGC AGA TCG TGG CAA GAA [ATG] GAC GGA
      -   L   L   L   E   G   R   S   W   Q   E   [M]   D   G

127 CAG AAG AAA CAT TGG AAG GAC AAG GTT GTT GAC CTC CTC TAC
      Q   K   K   H   W   K   D   K   V   V   D   L   L   Y

169 TGG AGA GAC ATT AAG AAG ACT GGA GTG GTG TTT GGT GCC AGC
      W   R   D   I   K   K   T   G   V   V   F   G   A   S

211 TTA TTC CTG CTG CTG TCT CTG ACA GTG TTC AGC ATT GTC AGT
      L   F   L   L   L   S   L   T   V   F   S   I   V   S

253 GTA ACG GCC TAC ATT GCC TTG GCC CTG CTC TCG GTG ACT ATC
      V   T   A   Y   I   A   L   A   L   L   S   V   T   I

295 AGC TTT AGG ATA TAT AAG GGC GTG ATC CAG GCT ATC CAG AAA
      S   F   R   I   Y   K   G   V   I   Q   A   I   Q   K

337 TCA GAT GAA GGC CAC CCA TTC AGG GCA TAT TTA GAA TCT GAA
      S   D   E   G   H   P   F   R   A   Y   L   E   S   E

379 GTT GCT ATA TCA GAG GAA TTG GTT CAG AAA TAC AGT AAT TCT
      V   A   I   S   E   E   L   V   Q   K   Y   S   N   S

421 GCT CTT GGT CAT GTG AAC AGC ACA ATA AAA GAA CTG AGG CGG
      A   L   G   H   V   N   S   T   I   K   E   L   R   R

463 CTT TTC TTA GTT GAT GAT TTA GTT GAT TCC CTG AAG TTT GCA
      L   F   L   V   D   D   L   V   D   S   L   K   F   A

505 GTG TTG ATG TGG GTG TTT ACT TAT GTT GGT GCC TTG TTC AAT
      V   L   M   W   V   F   T   Y   V   G   A   L   F   N

547 GGT CTG ACA CTA CTG ATT TTA GCT CTG ATC TCA CTC TTC AGT
      G   L   T   L   L   I   L   A   L   I   S   L   F   S
```

FIG. 14A

```
589  ATT CCT GTT ATT TAT GAA CGG CAT CAG GTG CAG ATA GAT CAT
       I   P   V   I   Y   E   R   H   Q   V   Q   I   D   H

631  TAT CTA GGA CTT GCA AAC AAG AGT GTT AAG GAT GCC ATG GCC
       Y   L   G   L   A   N   K   S   V   K   D   A   M   A

673  AAA ATC CAA GCA AAA ATC CCT GGA TTG AAG CGC AAA GCA GAT
       K   I   Q   A   K   I   P   G   L   K   R   K   A   D

     STOP
715  [TGA] AAA AGC CCC AAA CAG AAG TTC ATC TTT AAA GGG GAC ACT
       [-]   K   S   P   K   Q   K   F   I   F   K   G   D   T

757  CAC TTG ATT ACG GGG GTG GGA GGT CAG GGG TGA GCC CTT GGT
       H   L   I   T   G   V   G   G   Q   G   -   A   L   G

799  GGC CGT GCG GTT TCA GCT CTT TAT TTT TAG CAG TGC ACT GTT
       G   R   A   V   S   A   L   Y   F   -   Q   C   T   V

841  TGA GGA AAA ATT ACC TGT CTT GAC TTC CTG TGT TTA TCA TCT
       -   G   K   I   T   C   L   D   F   L   C   L   S   S

883  TAA GTA TTG TAA GCT GCT GTG TAT GGA TCT CAT TGT AGT CAC
       -   V   L   -   A   A   V   Y   G   S   H   C   S   H

925  ACT TGT CTT CCC CAA TGA GGC GCC TGG TGA ATA AAG GAC TCG
       T   C   L   P   Q   -   G   A   W   -   I   K   D   S

967  GGG AAA GCT GTG CAT TGT ATC TGC TGC AGG GTA GTC TAG CTG
       G   K   A   V   H   C   I   C   C   R   V   V   -   L

1009 TAT GCA GAG AGT TGT AAA GAA GGC AAA TCT GGG GGC AGG GAA
       Y   A   E   S   C   K   E   G   K   S   G   G   R   E

1051 AAC CCT TTT CAC AGT GTA CTG TGT TTG GTC AGT GTA AAA CTG
       N   P   F   H   S   V   L   C   L   V   S   V   K   L

1093 ATG CAG ATT TTT CTG AAA TGA AAT GTT TAG ATG AGA GCA TAC
       M   Q   I   F   L   K   -   N   V   -   M   R   A   Y

1135 TAC TAA AGC AGA GTG GAA AAC TCT GTC TTT ATG GTG TGT TCT
       Y   -   S   R   V   E   N   S   V   F   M   V   C   S
```

FIG. 14B

```
1177  AGG TGT ATT GTG AAT TTA CTG TTA TAT TGC CAA TAT AAG TAA
       R   C   I   V   N   L   L   L   Y   C   Q   Y   K   -

1219  ATA TAG ACC TAA TCT ATA TAT AGT GTT TCA CAA AGC TTA GAT
       I   -   T   -   S   I   Y   S   V   S   Q   S   L   D

1261  CTT TAA CCT TGC AGC TGC CCC ACA GTG CTT GAC CTC TGA GTC
       L   -   P   C   S   C   P   T   V   L   D   L   -   V

1303  ATT GGT TAT GCA GTG TAG TCC CAA GCA CAT AAA CTA GGA AGA
       I   G   Y   A   V   -   S   Q   A   H   K   L   G   R

1345  GAA ATG TAT TTG TAG GAG TGC TAC CTA CCA CCT GTT TTC AAG
       E   M   Y   L   -   E   C   Y   L   P   P   V   F   K

1387  AAA ATA TAG AAC TCC AAC AAA AAT ATA GAA TGT CAT TTC AAA
       K   I   -   N   S   N   K   N   I   E   C   H   F   K

1429  GAC TTA CTG TAT GTA TAG TTA ATT TTG TCA CAG ACT CTG AAA
       D   L   L   Y   V   -   L   I   L   S   Q   T   L   K

1471  TTC TAT GGA CTG AAT TTC ATG CTT CCA AAT GTT TGC AGT TAT
       F   Y   G   L   N   F   M   L   P   N   V   C   S   Y

1513  CAA ACA TTG TTA TGC AAG AAA TCA TAA AAT GAA GAC TTA TAC
       Q   T   L   L   C   K   K   S   -   N   E   D   L   Y

1555  CAT TGT GGT TTA AG
       H   C   G   L
```

FIG. 14C

FIG.15A FIG.15B

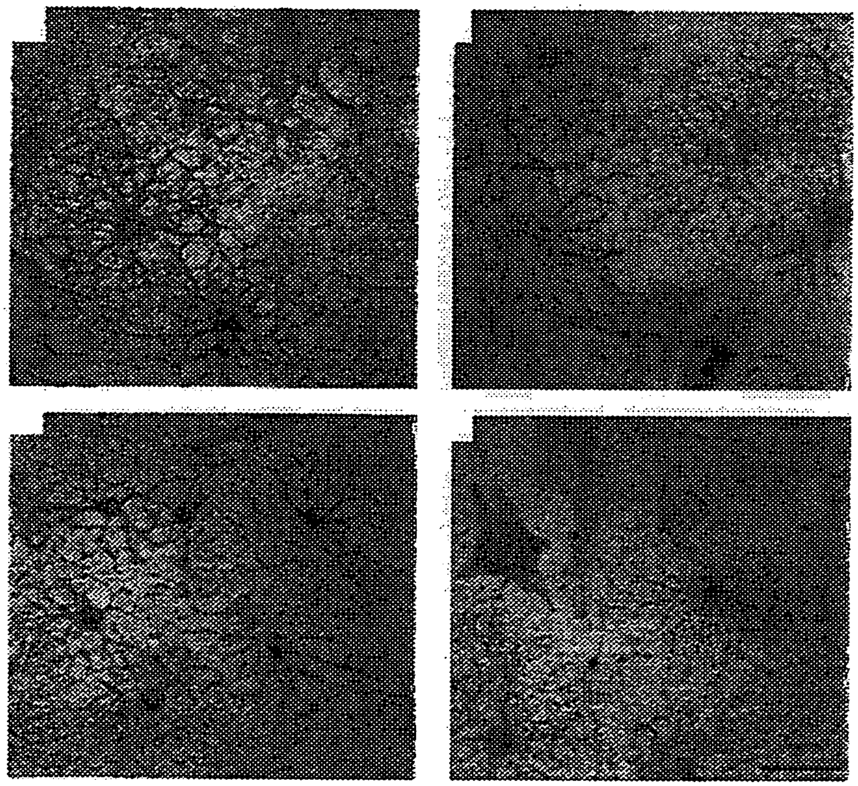


FIG.15C FIG.15D

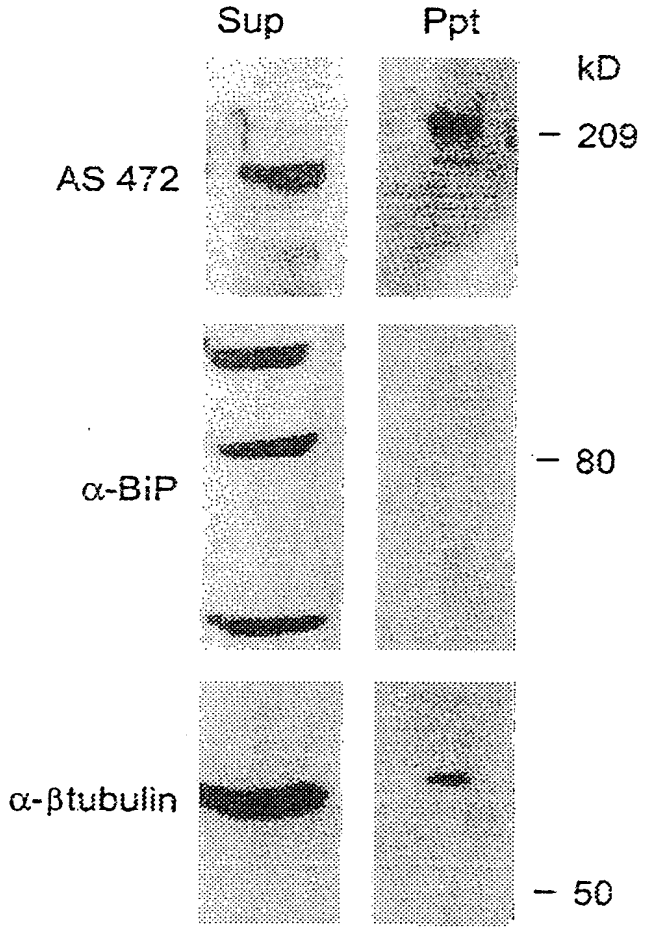


FIG. 15E

FIG.16A

FIG.16B

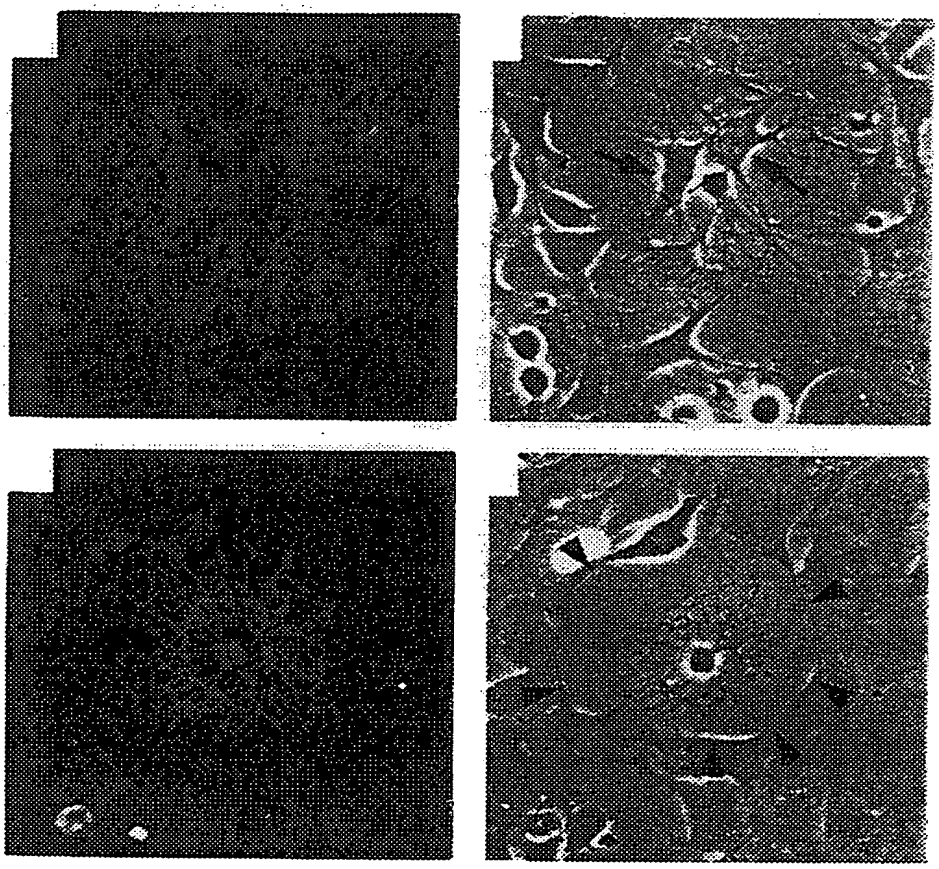


FIG.16C

FIG.16D

FIG.16E

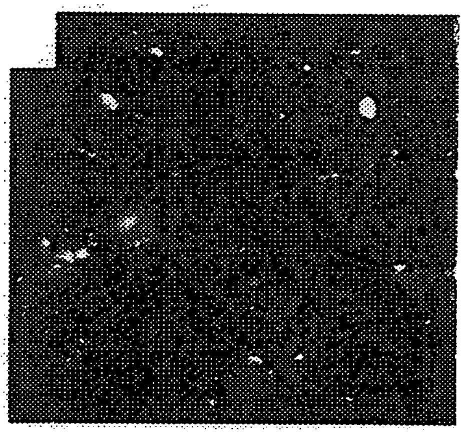
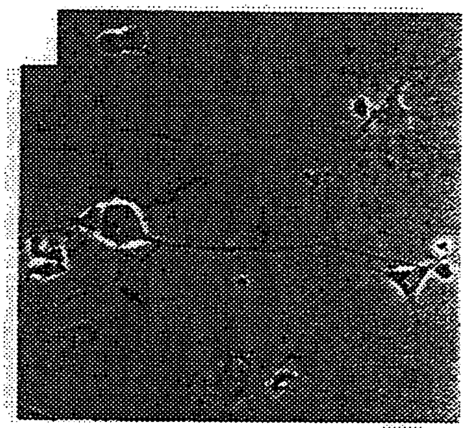


FIG.16F



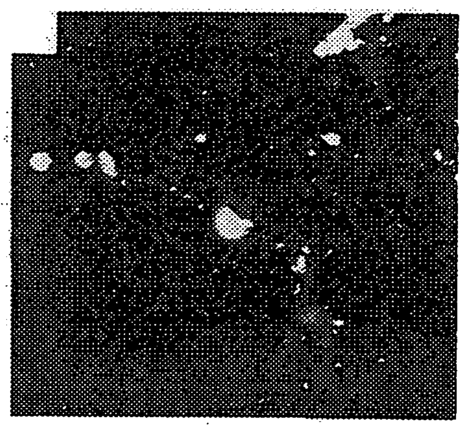


FIG.16G

FIG.16H

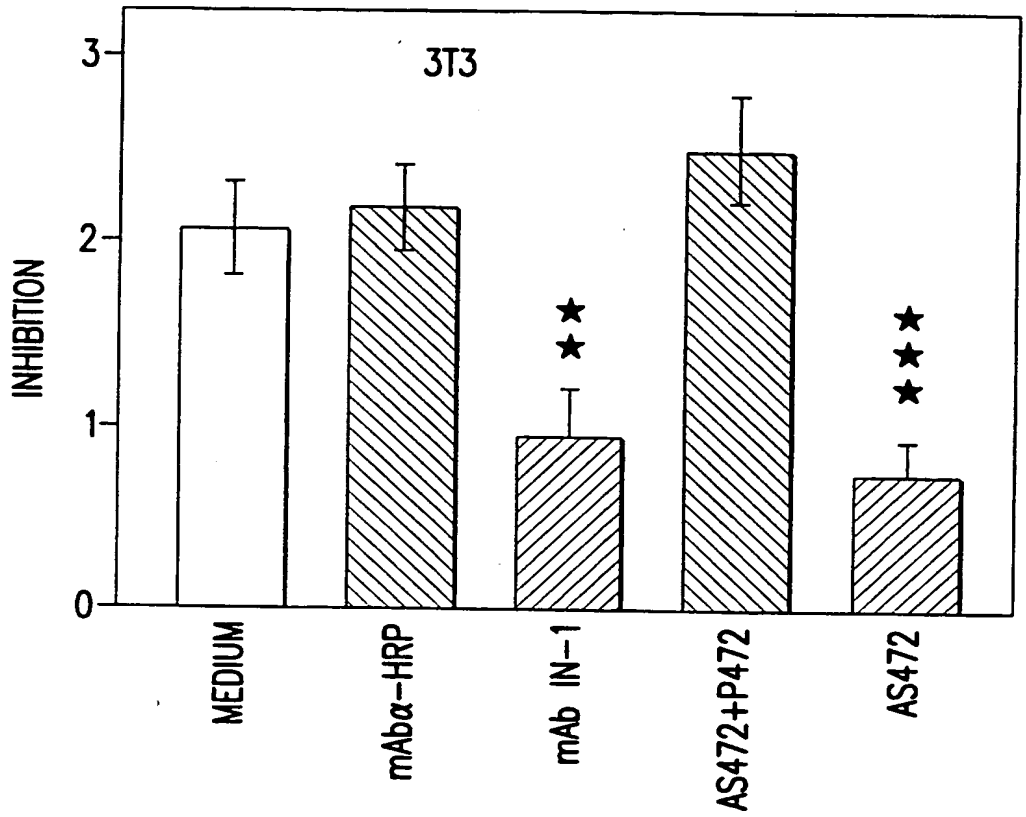


FIG.16I

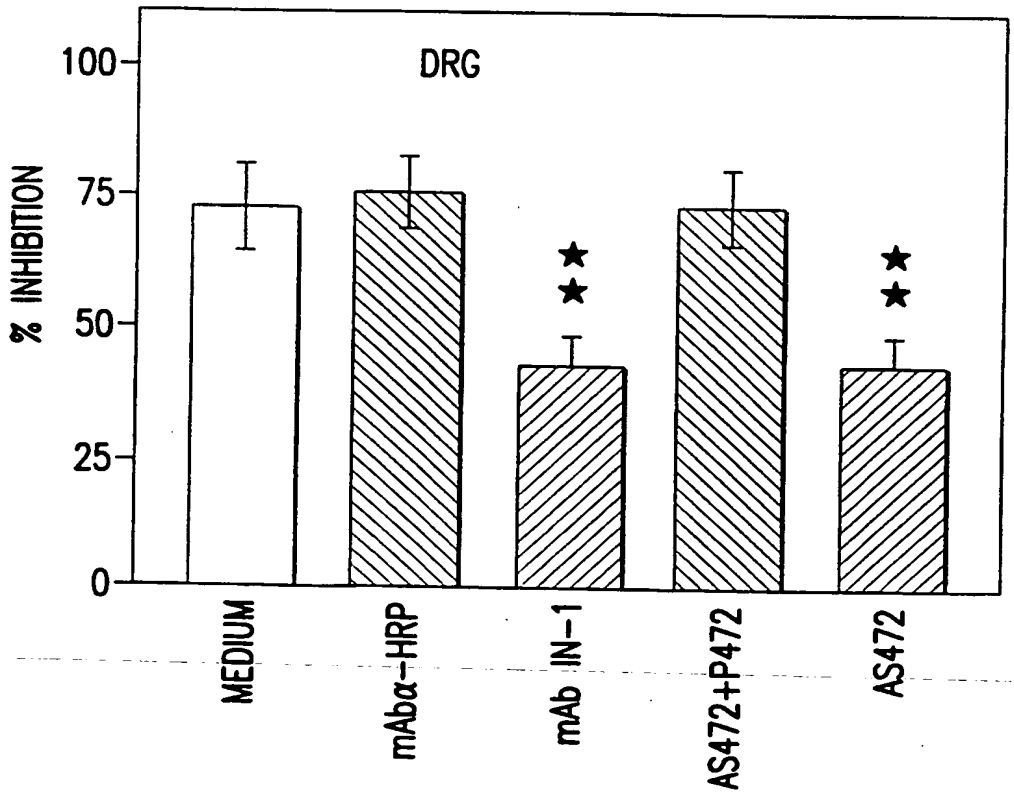


FIG.16J

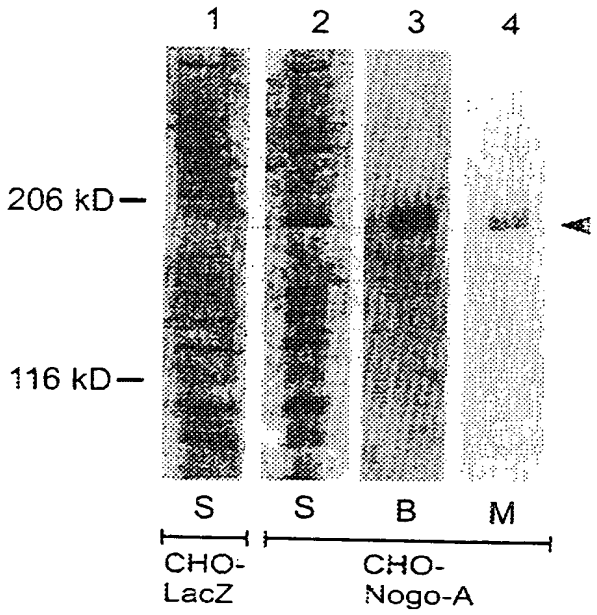


FIG. 17A

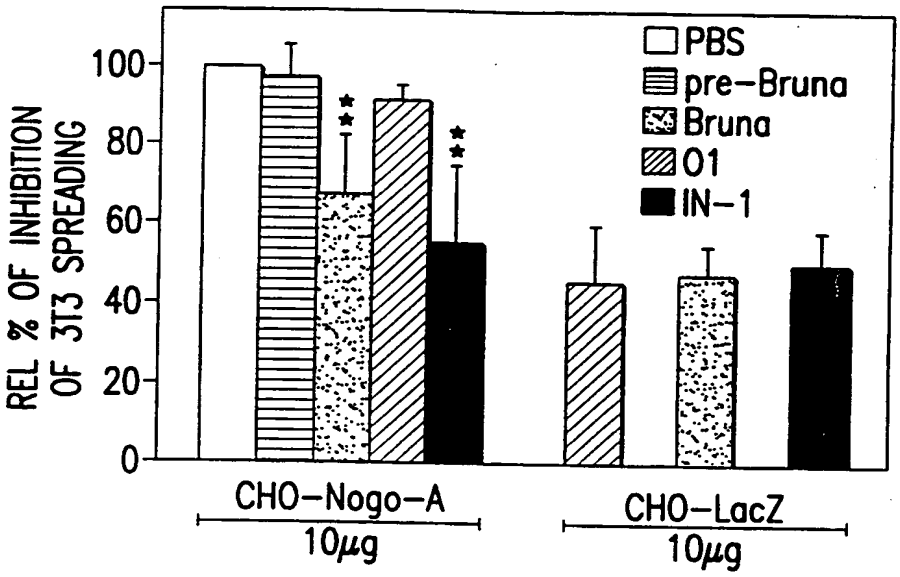


FIG. 17B

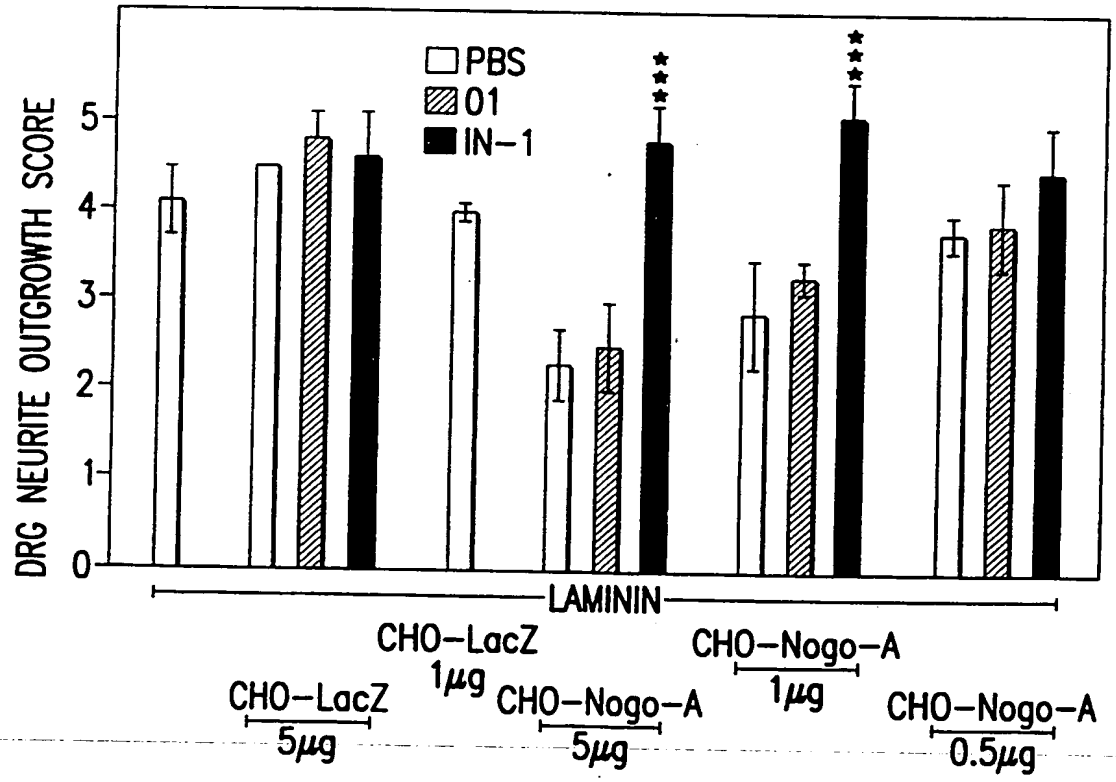


FIG. 17C

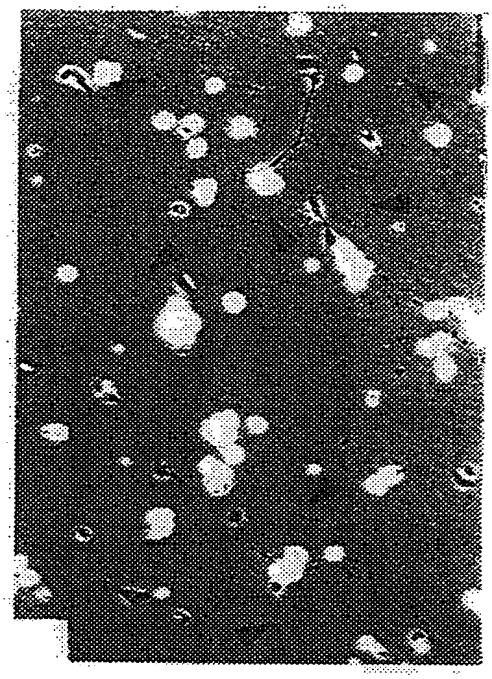


FIG.17E

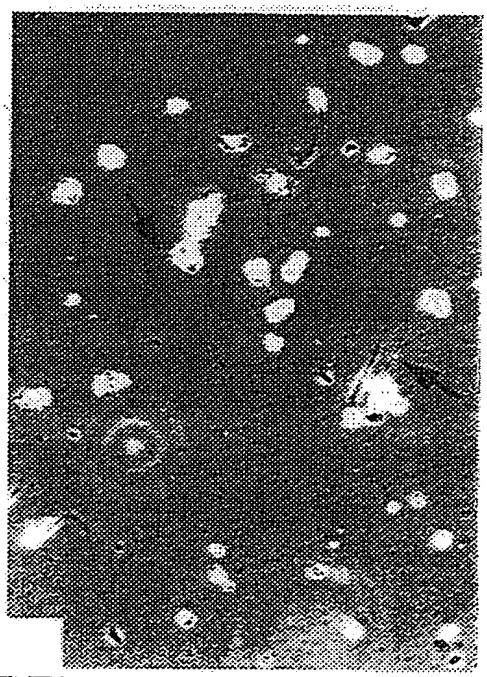
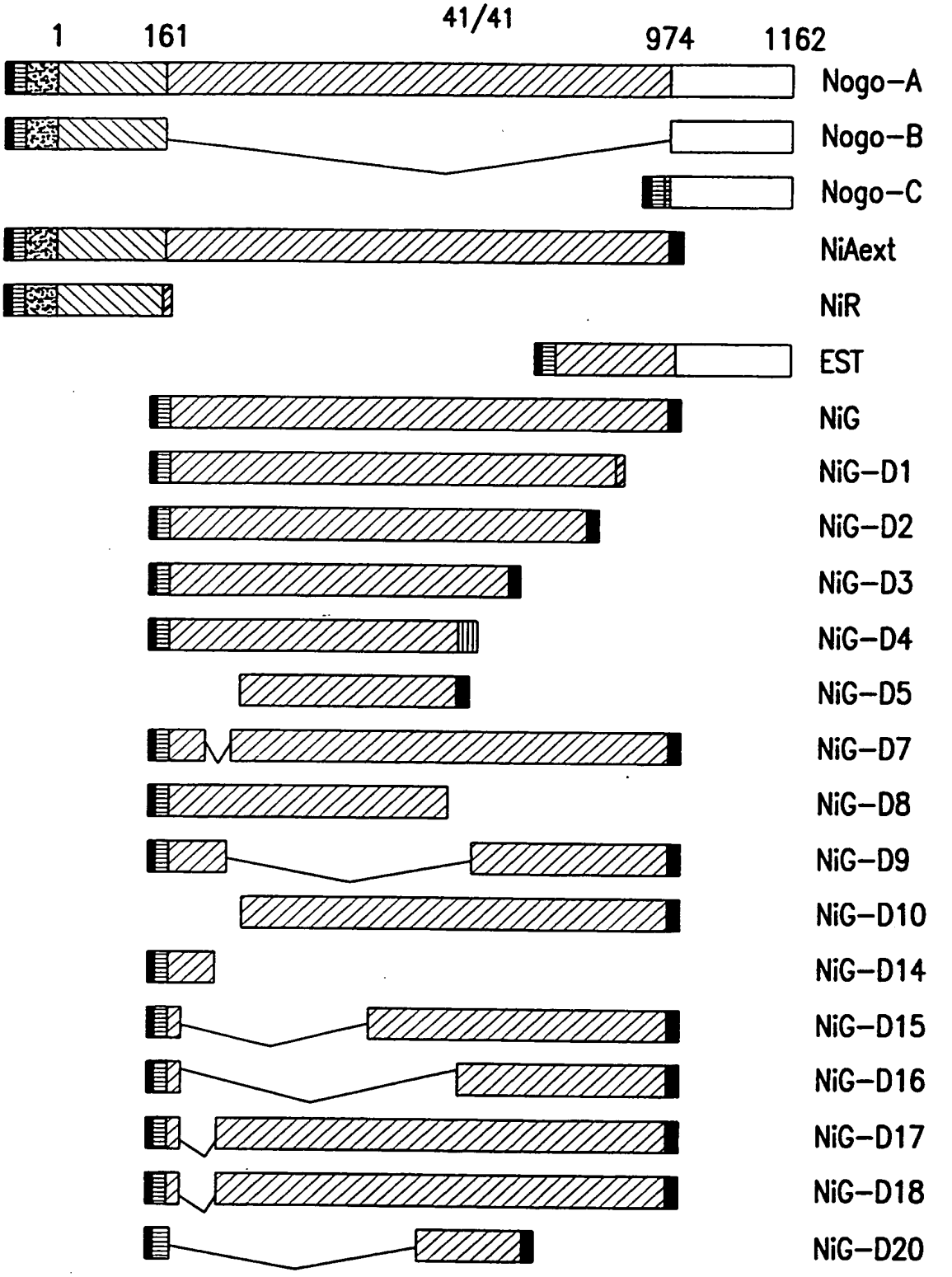


FIG.17D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Nogo-B
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EST
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NiG-D5
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His-tag
N-TERMINAL VECTOR SEQUENCE
Nogo-C-SPECIFIC N-TERMINAL SEQUENCE
T7-tag
C-TERMINAL VECTOR SEQUENCES

FIG. 18